

SEQUENCE LISTING

<110> Jukka T. SALONEN et al.

<120> METHOD FOR DETECTING THE RISK OF CARDIOVASCULAR DISEASES SUCH AS ACUTE MYOCARDIAL INFARCTION AND CORONARY HEART DISEASE BY ANALYSING DEFENSIN

<130> 0933-0279PUS1

<140> US 10/586,312

<141> 2006-07-14

<160> 56

<170> PatentIn version 3.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

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cataatttca gcccgatgtg 20

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<211> 20

<212> DNA

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<220>

<223> Description of Artificial Sequence: PCR primer

<400> 2

caccctaacc ccctacttct 20

<210> 3

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<220>

<223> Description of Artificial Sequence: PCR primer

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gggcttgctc tttctttc 18

<210> 4

<211> 18

<212> DNA

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<220>
 <223> Description of Artificial Sequence: PCR primer

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 tccttggttc ctctcatc 18

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<220>
 <223> Description of Artificial Sequence: PCR primer

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 ctgagtgtgc aggacgag 18

<210> 6
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<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 6
 cacattgcc aacacgat 18

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 <213> Homo sapiens

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 agaaagagga gcatcaaagg gatcttgaga acaaaggcag tccttcccct cccaatcaca 60
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 caggctgact cctcactccc cacatatcca ctctgtctct ccctcctgca ggtgacccca 180
 gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct 240
 gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac 300
 caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg 360
 agacatcaat cttgcacatc tgcaaaatct agaaaaaag gattggagaa aggatctgga 420
 gtcaagtgtg gaaaggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga 480
 ttttctcatc tataaattaa tcagtgagaa ccaaataaat ctaaaagatt ttcttttttc 540
 taagactttc agttccaaga tatttctgtg aaatttgcta cttttaagat agaaagacct 600

acactgacta gttctttgta gatctaaatg ggcagactta gttatataga gagtgtttta	660
ctttgtccat tggaaaagct tttagaacct agagaggaac ctataggtgt gttttgatgt	720
aggctaatag gcttga	736

<210> 8
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 <212> DNA
 <213> Homo sapiens

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tgcccacctc ctctcactgc agcttctgtc tcaggtcttc tcccagcaga gctataaatc	120
caggctgact cctcactccc cacatatcca ctctgctct cctcctgca ggtgacccca	180
gccatgagga ccatcgccat ctttgctgcc attctcctgg tggccctgca ggcccaggct	240
gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac	300
caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg	360
agacatcaat cttgcacatc tgcaaaatct agaaaaaag gattggagaa aggatctgga	420
gtcaagtgtg gaaaggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga	480
ttttctcatc tataaattaa tcagtgagaa ccaaataaat ctaaaagatt ttcttttttc	540
taagactttc agctccaaga tatttctgtg aaatttgcta cttttaagat agaaagagct	600
acactgacta gttctttgta gatctaaatg ggcagactta gttatataga gagtgtttta	660
ctttgtccat tggaaaagct tttagaacct agagaggaac ctataggtgt gttttgatgt	720
aggctaatag gcttga	736

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 9	
agaaagagga gcatcaaag	19

<210> 10
 <211> 19
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<220>
 <223> Description of Artificial Sequence: PCR primer

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 tcaagcctat tagcctaca 19

 <210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 11
 gacaacctca atgctctgct 20

 <210> 12
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 12
 tgacttacct ggacatggct 20

 <210> 13
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 13
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 <210> 14
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

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 <210> 15

<211> 45
 <212> DNA
 <213> Artificial Sequence

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 <212> DNA
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 <220>
 <223> Snapshot primer

 <400> 16
 tttttttttt tttttttttt tttttttttt tttccagaga ggaagccttg 50

 <210> 17
 <211> 55
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

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 <210> 18
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 18
 tttttttttt tttttttttt tttttttttt tttttttttt tttaccacga cgtcacgcag 60

 <210> 19
 <211> 30
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 <213> Artificial Sequence

 <220>
 <223> Snapshot primer

 <400> 19
 tttttttttt tttgaagacc agccagtgca 30

<210> 20
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> Coding sequence for variant human ADRA2B gene

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 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc gcc aac gct ctg 96
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
 Leu Phe Leu Val Ser Leu Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg gcc tac tgg tac ttc 240
 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc 384
 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg 432
 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

ctg ccg ccc ctc atc tac aag gcc gac cag gcc ccc cag ccg cgc ggg 480
 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc 528
 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
 165 170 175

agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac	576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr	
180 185 190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg	624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg	
195 200 205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac	672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp	
210 215 220	
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg	720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val	
225 230 235 240	
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys	
245 250 255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu	
290 295 300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc	960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys	
305 310 315 320	
agc ccc ccg ctg cag cag cca cag ggc tcc ccg gtg ctg gcc acc cta	1008
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu	
325 330 335	
cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag	1056
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln	
340 345 350	
tgg tgg cgt cga agg gcg cac gtg acc ccg gag aag cgc ttc acc ttc	1104
Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe	
355 360 365	
gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc	1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe	
370 375 380	
ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg	1200
Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val	
385 390 395 400	
ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc	1248

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
 420 425 430

gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
 Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
 435 440 445

<210> 21
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 21

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
 115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
 130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
 145 150 155 160

Arg	Pro	Gln	Cys	Lys	Leu	Asn	Gln	Glu	Ala	Trp	Tyr	Ile	Leu	Ala	Ser			
				165					170					175				
Ser	Ile	Gly	Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr			
			180					185					190					
Leu	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Arg	Ser	Asn	Arg	Arg	Gly	Pro	Arg			
		195					200					205						
Ala	Lys	Gly	Gly	Pro	Gly	Gln	Gly	Glu	Ser	Lys	Gln	Pro	Arg	Pro	Asp			
	210					215					220							
His	Gly	Gly	Ala	Leu	Ala	Ser	Ala	Lys	Leu	Pro	Ala	Leu	Ala	Ser	Val			
225					230					235					240			
Ala	Ser	Ala	Arg	Glu	Val	Asn	Gly	His	Ser	Lys	Ser	Thr	Gly	Glu	Lys			
				245					250					255				
Glu	Glu	Gly	Glu	Thr	Pro	Glu	Asp	Thr	Gly	Thr	Arg	Ala	Leu	Pro	Pro			
			260					265					270					
Ser	Trp	Ala	Ala	Leu	Pro	Asn	Ser	Gly	Gln	Gly	Gln	Lys	Glu	Gly	Val			
		275					280					285						
Cys	Gly	Ala	Ser	Pro	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Glu			
	290					295					300							
Glu	Glu	Cys	Glu	Pro	Gln	Ala	Val	Pro	Val	Ser	Pro	Ala	Ser	Ala	Cys			
305					310					315					320			
Ser	Pro	Pro	Leu	Gln	Gln	Pro	Gln	Gly	Ser	Arg	Val	Leu	Ala	Thr	Leu			
				325					330					335				
Arg	Gly	Gln	Val	Leu	Leu	Gly	Arg	Gly	Val	Gly	Ala	Ile	Gly	Gly	Gln			
			340					345					350					
Trp	Trp	Arg	Arg	Arg	Ala	His	Val	Thr	Arg	Glu	Lys	Arg	Phe	Thr	Phe			
		355					360					365						
Val	Leu	Ala	Val	Val	Ile	Gly	Val	Phe	Val	Leu	Cys	Trp	Phe	Pro	Phe			
	370					375					380							

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
 385 390 395 400

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
 405 410 415

Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
 420 425 430

Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
 435 440 445

<210> 22
 <211> 1353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> Coding sequence for human ADRA2B gene

<400> 22
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 Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15
 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg 96
 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30
 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144
 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45
 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60
 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
 65 70 75 80
 cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
 85 90 95
 acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg 336
 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
 100 105 110

gcc	gtg	agc	cgc	gcg	ctg	gag	tac	aac	tcc	aag	cgc	acc	ccg	cgc	cgc	384
Ala	Val	Ser	Arg	Ala	Leu	Glu	Tyr	Asn	Ser	Lys	Arg	Thr	Pro	Arg	Arg	
		115					120					125				
atc	aag	tgc	atc	atc	ctc	act	gtg	tgg	ctc	atc	gcc	gcc	gtc	atc	tcg	432
Ile	Lys	Cys	Ile	Ile	Leu	Thr	Val	Trp	Leu	Ile	Ala	Ala	Val	Ile	Ser	
	130					135					140					
ctg	ccg	ccc	ctc	atc	tac	aag	ggc	gac	cag	ggc	ccc	cag	ccg	cgc	ggg	480
Leu	Pro	Pro	Leu	Ile	Tyr	Lys	Gly	Asp	Gln	Gly	Pro	Gln	Pro	Arg	Gly	
145					150					155					160	
cgc	ccc	cag	tgc	aag	ctc	aac	cag	gag	gcc	tgg	tac	atc	ctg	gcc	tcc	528
Arg	Pro	Gln	Cys	Lys	Leu	Asn	Gln	Glu	Ala	Trp	Tyr	Ile	Leu	Ala	Ser	
				165					170					175		
agc	atc	gga	tct	ttc	ttt	gct	cct	tgc	ctc	atc	atg	atc	ctt	gtc	tac	576
Ser	Ile	Gly	Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr	
			180					185					190			
ctg	cgc	atc	tac	ctg	atc	gcc	aaa	cgc	agc	aac	cgc	aga	ggc	ccc	agg	624
Leu	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Arg	Ser	Asn	Arg	Arg	Gly	Pro	Arg	
		195					200					205				
gcc	aag	ggg	ggg	cct	ggg	cag	ggc	gag	tcc	aag	cag	ccc	cga	ccc	gac	672
Ala	Lys	Gly	Gly	Pro	Gly	Gln	Gly	Glu	Ser	Lys	Gln	Pro	Arg	Pro	Asp	
	210					215					220					
cat	ggc	ggg	gct	ttg	gcc	tca	gcc	aaa	ctg	cca	gcc	ctg	gcc	tct	gtg	720
His	Gly	Gly	Ala	Leu	Ala	Ser	Ala	Lys	Leu	Pro	Ala	Leu	Ala	Ser	Val	
225					230					235					240	
gct	tct	gcc	aga	gag	gtc	aac	gga	cac	tcg	aag	tcc	act	ggg	gag	aag	768
Ala	Ser	Ala	Arg	Glu	Val	Asn	Gly	His	Ser	Lys	Ser	Thr	Gly	Glu	Lys	
				245					250					255		
gag	gag	ggg	gag	acc	cct	gaa	gat	act	ggg	acc	cgg	gcc	ttg	cca	ccc	816
Glu	Glu	Gly	Glu	Thr	Pro	Glu	Asp	Thr	Gly	Thr	Arg	Ala	Leu	Pro	Pro	
			260					265					270			
agt	tgg	gct	gcc	ctt	ccc	aac	tca	ggc	cag	ggc	cag	aag	gag	ggc	gtt	864
Ser	Trp	Ala	Ala	Leu	Pro	Asn	Ser	Gly	Gln	Gly	Gln	Lys	Glu	Gly	Val	
		275					280					285				
tgt	ggg	gca	tct	cca	gag	gat	gaa	gct	gaa	gag	gag	gaa	gag	gag	gag	912
Cys	Gly	Ala	Ser	Pro	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
	290					295					300					
gag	gag	gag	gaa	gag	tgt	gaa	ccc	cag	gca	gtg	cca	gtg	tct	ccg	gcc	960
Glu	Glu	Glu	Glu	Glu	Cys	Glu	Pro	Gln	Ala	Val	Pro	Val	Ser	Pro	Ala	
305					310					315					320	
tca	gct	tgc	agc	ccc	ccg	ctg	cag	cag	cca	cag	ggc	tcc	cgg	gtg	ctg	1008
Ser	Ala	Cys	Ser	Pro	Pro	Leu	Gln	Gln	Pro	Gln	Gly	Ser	Arg	Val	Leu	
				325					330					335		

gcc acc cta cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata 1056
 Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350

ggt ggg cag tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc 1104
 Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
 355 360 365

ttc acc ttc gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg 1152
 Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380

ttc ccc ttc ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac 1200
 Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
 385 390 395 400

tgc aag gtg ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac 1248
 Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415

tgc aac agc tca ctg aac cct gtt atc tac acc atc ttc aac cag gac 1296
 Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
 420 425 430

ttc cgc cgt gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg 1344
 Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
 435 440 445

gcc tgg tga 1353
 Ala Trp
 450

<210> 23
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 23

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
 1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
 20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
 35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
 50 55 60

Ile	Ile	Pro	Phe	Ser	Leu	Ala	Asn	Glu	Leu	Leu	Gly	Tyr	Trp	Tyr	Phe	65	70	75	80
Arg	Arg	Thr	Trp	Cys	Glu	Val	Tyr	Leu	Ala	Leu	Asp	Val	Leu	Phe	Cys	85	90	95	
Thr	Ser	Ser	Ile	Val	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Trp	100	105	110	
Ala	Val	Ser	Arg	Ala	Leu	Glu	Tyr	Asn	Ser	Lys	Arg	Thr	Pro	Arg	Arg	115	120	125	
Ile	Lys	Cys	Ile	Ile	Leu	Thr	Val	Trp	Leu	Ile	Ala	Ala	Val	Ile	Ser	130	135	140	
Leu	Pro	Pro	Leu	Ile	Tyr	Lys	Gly	Asp	Gln	Gly	Pro	Gln	Pro	Arg	Gly	145	150	155	160
Arg	Pro	Gln	Cys	Lys	Leu	Asn	Gln	Glu	Ala	Trp	Tyr	Ile	Leu	Ala	Ser	165	170	175	
Ser	Ile	Gly	Ser	Phe	Phe	Ala	Pro	Cys	Leu	Ile	Met	Ile	Leu	Val	Tyr	180	185	190	
Leu	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Arg	Ser	Asn	Arg	Arg	Gly	Pro	Arg	195	200	205	
Ala	Lys	Gly	Gly	Pro	Gly	Gln	Gly	Glu	Ser	Lys	Gln	Pro	Arg	Pro	Asp	210	215	220	
His	Gly	Gly	Ala	Leu	Ala	Ser	Ala	Lys	Leu	Pro	Ala	Leu	Ala	Ser	Val	225	230	235	240
Ala	Ser	Ala	Arg	Glu	Val	Asn	Gly	His	Ser	Lys	Ser	Thr	Gly	Glu	Lys	245	250	255	
Glu	Glu	Gly	Glu	Thr	Pro	Glu	Asp	Thr	Gly	Thr	Arg	Ala	Leu	Pro	Pro	260	265	270	
Ser	Trp	Ala	Ala	Leu	Pro	Asn	Ser	Gly	Gln	Gly	Gln	Lys	Glu	Gly	Val	275	280	285	

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
 290 295 300

Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
 305 310 315 320

Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
 325 330 335

Ala Thr Leu Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile
 340 345 350

Gly Gly Gln Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg
 355 360 365

Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp
 370 375 380

Phe Pro Phe Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His
 385 390 395 400

Cys Lys Val Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr
 405 410 415

Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp
 420 425 430

Phe Arg Arg Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr
 435 440 445

Ala Trp
 450

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 24
 gggtgtttgt ggggcatctc

20

<210> 25

<211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Snapshot primer

<400> 25
 tggcactgcc tgggggttca 19

<210> 26
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequencing primer

<400> 26
 tcaggtcttc tcccagca 18

<210> 27
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 27
 ggatgaagca gaatgaagag taggtaaccc tgaggttgag aggtatatattg ttggaccagg 60
 gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120
 tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
 atcctaacat gactgataca gtgtctctta tttagactat ctcagttagt ctggctgtgc 240
 ttgtcctttt tcccacctcc ctgctgtgc ctgacctct cttctttcca caggttctca 300
 ggcaagagcc acctgctatt gccgaaccgg ccgttggtgt acctgtgagt ccctctccgg 360
 ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
 aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480
 gtaccttggtg tcttttctaaa tttctctctc caaagtaaag ttcaagcatt aaacttagtg 540
 tgtttgacct ttttaatttt cttttctttt tccttttttt tcttttgctt tgttatatgg 600
 tggtttgtat ggttccttt 619

<210> 28
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 28
ggatgaagca gaatgaagag taggtaaccc tgaggttgag aggtatattg ttggaccagg 60
gagcaggtaa taaatacatc ctggatagac tcacatgggg aaaaaaacta tgatcttgca 120
tgactaacac atagctagta agatttcttg tcacttacga caaagacatg aattttctcc 180
atcctaacat gactgataca gtgtctctta tttagactat ctcagttagt ctggctgtgc 240
ttgtcctttt tcccacctcc ctgctgtgc ctgaccctct cttctttcca caggttctca 300
ggcaagagcc acctgctatt gccgaaccgg ccgttgtgct acccgtgagt ccctctccgg 360
ggtgtgtgaa atcagtggcc gcctctacag actctgctgt cgctgagctt cctagataga 420
aaccaaagca gtgcaagatt cagttcaagg tcctgaaaaa agaaaaacat tttactctgt 480
gtaccttggtg tctttctaaa tttctctctc caaaataaag ttcaagcatt aaacttagtg 540
tgtttgacct ttttaatttt cttttctttt tccctttttt tcttttgctt tgttatatgg 600
tggtttgtat ggttccttt 619

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 29
ggatgaagca gaatgaaga 19

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 30
aaaggaacca taaaacca 19

<210> 31
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequencing primer

<400> 31

gtagtctgg ctgtgctt

18

<210> 32
<211> 1052
<212> DNA
<213> Homo sapiens

<400> 32
gggctactga gtttgggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60
cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120
ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc 180
catcctaaaa gcaaataatt actctatcat ctacgtgcc tttgcttctt aaagttactc 240
aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct 300
cagcctgccc atttgccctt atcaacattc ctaaacactg ggcttaaaat gtagtatgag 360
taaactctct cttagtctat ccatctccca ctagcagttt taacatcatc tctagttatt 420
aaccttggct caatggcttt ctctctttt ttatacaga atttattggc ttgagacgct 480
gtttaatggg tttggggaga tgcagggatc actgcaatgt ggatgaaaaa gagatacaga 540
aatgcaagat gaaaaaatgt tgtgttggac caaaagtgg taaattgatt aaaaactacc 600
tgcaatatgg aacaccaa atgtacttaatg aagacgtcca agaaatgcta aaacctgcca 660
agaattctag tgctgtgata caaagaaaac atatcttctc tgttctcccc caaatcaaaa 720
gcactagctt ttttgcta atcaactttg tcatcattcc aaatgccacc cctatgaact 780

ctgccaccat cagcactatg accccaggac agatcacata cactgctact tctaccaaga 840
gtaacaccaa agaaagcaga gattctgcca ctgcctcgcc accaccagca ccacctccac 900
caaacatact gccaacacca tcaactggagc tagaggaagc agaagagcag taatgtggat 960
ctttccctta aaactccaag ttcctctcta tttttgctat ctataaaatg acatagaact 1020
gtttcctctg tcatcagtca ttcaataaac ac 1052

<210> 33
<211> 1049
<212> DNA
<213> Homo sapiens

<400> 33
gggctactga gtttgggtgaa aagataagac tcctgaaaat tctattgatt ctcttttgaa 60
cttcttttctt aaattagttt tatgatggac ttggctctca ttggtatttc ccaagattat 120

ggagatggga tagtgatgtc tgacaagtac ctaagatgct aagttgaagg tctaaaattc	180
catcctaaaa gcaaataatt actctatcat ctacgtgccc ttgcttctt aaagttactc	240
aaggaaggca gactaaacag gaaatttact ttggattcaa gaggggcata gagacgctct	300
cagcctgccc atttgccttc atcaacattc ctaaacactg ggcttaaaat gtagtatgag	360
taaactctct cttagtctat ccattctcca ctagcagttt taacatcatc tctagttatt	420
aaccttggct caatggcttt ctcttttttt atacagaatt tattggcttg agacgctggt	480
taatgggttt ggggagatgc agggatcact gcaatgtgga tgaaaaagag atacagaaat	540
gcaagatgaa aaaatgttgt gttggaccaa aagtgggtta attgattaaa aactacctgc	600
aatatggaac accaaatgta cttaatgaag acgtccaaga aatgctaaaa cctgccaaga	660
attctagtgc tgtgatacaa agaaaacata ttttatctgt tctcccccaa atcaaaagca	720
ctagcttttt tgctaatacc aactttgtca tcattccaaa tgccaccctt atgaactctg	780
ccaccatcag cactatgacc ccaggacaga tcacatacac tgctacttct accaagagta	840
acaccaaaga aagcagagat tctgccactg cctcgccacc accagcacca cctccaccaa	900
acatactgcc aacaccatca ctggagctag aggaagcaga agagcagtaa tgtggatctt	960
tcccttaaaa ctccaagttc ctctctatct ttgctatcta taaaatgaca tagaactgtt	1020
tcctctgtca tcagtcattc aataaacac	1049

<210> 34
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 34	
ggctactgag ttggtga	18

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 35	
gtgtttattg aatgactgat g	21

<210> 36
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequencing primer

<400> 36
 caaggaaggc agactaaa 18

<210> 37
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the variant human DEFB129 gene

<400> 37
 atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15

gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30

aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45

aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60

aac tac ctg caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80

gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95

cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110

aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125

acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432
 Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser

130		135		140	
acc aag agt aac acc aaa gaa agc aga gat tct gcc act gcc tcg cca					480
Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro					
145		150		155	160
cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg gag					528
Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu					
		165		170	175
cta gag gaa gca gaa gag cag taa					552
Leu Glu Glu Ala Glu Glu Gln					
		180			

<210> 38
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
1 5 10 15

Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
20 25 30

Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser
130 135 140

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 39
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(552)
 <223> Coding sequence for the human DEFB129 gene

<400> 39
 atg aag ctc ctt ttt cct atc ttt gcc agc ctc atg cta cag tac cag 48
 Met Lys Leu Leu Phe Pro Ile Phe Ala Ser Leu Met Leu Gln Tyr Gln
 1 5 10 15
 gtg aac aca gaa ttt att ggc ttg aga cgc tgt tta atg ggt ttg ggg 96
 Val Asn Thr Glu Phe Ile Gly Leu Arg Arg Cys Leu Met Gly Leu Gly
 20 25 30
 aga tgc agg gat cac tgc aat gtg gat gaa aaa gag ata cag aaa tgc 144
 Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys
 35 40 45
 aag atg aaa aaa tgt tgt gtt gga cca aaa gtg gtt aaa ttg att aaa 192
 Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys
 50 55 60
 aac tac cta caa tat gga aca cca aat gta ctt aat gaa gac gtc caa 240
 Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln
 65 70 75 80
 gaa atg cta aaa cct gcc aag aat tct agt gct gtg ata caa aga aaa 288
 Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys
 85 90 95
 cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt gct 336
 His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala
 100 105 110
 aat acc aac ttt gtc atc att cca aat gcc acc cct atg aac tct gcc 384
 Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala
 115 120 125
 acc atc agc act atg acc cca gga cag atc aca tac act gct act tct 432

Thr	Ile	Ser	Thr	Met	Thr	Pro	Gly	Gln	Ile	Thr	Tyr	Thr	Ala	Thr	Ser		
130						135					140						
acc	aag	agt	aac	acc	aaa	gaa	agc	aga	gat	tct	gcc	act	gcc	tcg	cca	480	
Thr	Lys	Ser	Asn	Thr	Lys	Glu	Ser	Arg	Asp	Ser	Ala	Thr	Ala	Ser	Pro		
145					150					155					160		
cca	cca	gca	cca	cct	cca	cca	aac	ata	ctg	cca	aca	cca	tca	ctg	gag	528	
Pro	Pro	Ala	Pro	Pro	Pro	Pro	Asn	Ile	Leu	Pro	Thr	Pro	Ser	Leu	Glu		
				165					170					175			
cta	gag	gaa	gca	gaa	gag	cag	taa									552	
Leu	Glu	Glu	Ala	Glu	Glu	Gln											
			180														

<210> 40
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 40

Met	Lys	Leu	Leu	Phe	Pro	Ile	Phe	Ala	Ser	Leu	Met	Leu	Gln	Tyr	Gln
1				5					10					15	

Val	Asn	Thr	Glu	Phe	Ile	Gly	Leu	Arg	Arg	Cys	Leu	Met	Gly	Leu	Gly
			20					25					30		

Arg	Cys	Arg	Asp	His	Cys	Asn	Val	Asp	Glu	Lys	Glu	Ile	Gln	Lys	Cys
		35					40					45			

Lys	Met	Lys	Lys	Cys	Cys	Val	Gly	Pro	Lys	Val	Val	Lys	Leu	Ile	Lys
	50					55					60				

Asn	Tyr	Leu	Gln	Tyr	Gly	Thr	Pro	Asn	Val	Leu	Asn	Glu	Asp	Val	Gln
65					70					75					80

Glu	Met	Leu	Lys	Pro	Ala	Lys	Asn	Ser	Ser	Ala	Val	Ile	Gln	Arg	Lys
				85					90					95	

His	Ile	Leu	Ser	Val	Leu	Pro	Gln	Ile	Lys	Ser	Thr	Ser	Phe	Phe	Ala
			100					105					110		

Asn	Thr	Asn	Phe	Val	Ile	Ile	Pro	Asn	Ala	Thr	Pro	Met	Asn	Ser	Ala
		115					120					125			

Thr	Ile	Ser	Thr	Met	Thr	Pro	Gly	Gln	Ile	Thr	Tyr	Thr	Ala	Thr	Ser
130						135					140				

Thr Lys Ser Asn Thr Lys Glu Ser Arg Asp Ser Ala Thr Ala Ser Pro
 145 150 155 160

Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu Glu
 165 170 175

Leu Glu Glu Ala Glu Glu Gln
 180

<210> 41
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence for the variant human DEFB118 gene

<400> 41
 atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15
 gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30
 cac cgc agg aaa caa tgc aaa gat gga gaa gca gtg aaa gat aca tgc 144
 His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45
 aaa aat ctt cga gct tgc tgc att cca tcc aat gaa gac cac agg cga 192
 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60
 gtt cct gcg aca tct ccc aca ccc ttg agt gac tca aca cca gga att 240
 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80
 att gat gat att tta aca gta agg ttc acg aca gac tac ttt gaa gta 288
 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95
 agc agc aag aaa gat atg gtt gaa gag tct gag gcg gga agg gga act 336
 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110
 gag acc tct ctt cca aat gtt cac cat agc tca tga 372
 Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 42
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 42

Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly
 20 25 30

His Arg Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys
 35 40 45

Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg
 50 55 60

Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile
 65 70 75 80

Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val
 85 90 95

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
 100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
 115 120

<210> 43
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(372)
 <223> Coding sequence of the human DEFB118 gene

<400> 43

atg aaa ctc ctg ctg ctg gct ctt cct atg ctt gtg ctc cta ccc caa 48
 Met Lys Leu Leu Leu Leu Ala Leu Pro Met Leu Val Leu Leu Pro Gln
 1 5 10 15

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg 96
 Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp Asn Arg Ser Gly

20					25					30						
cac	tgc	agg	aaa	caa	tgc	aaa	gat	gga	gaa	gca	gtg	aaa	gat	aca	tgc	144
His	Cys	Arg	Lys	Gln	Cys	Lys	Asp	Gly	Glu	Ala	Val	Lys	Asp	Thr	Cys	
		35					40					45				
aaa	aat	ctt	cga	gct	tgc	tgc	att	cca	tcc	aat	gaa	gac	cac	agg	cga	192
Lys	Asn	Leu	Arg	Ala	Cys	Cys	Ile	Pro	Ser	Asn	Glu	Asp	His	Arg	Arg	
	50					55					60					
gtt	cct	gcg	aca	tct	ccc	aca	ccc	ttg	agt	gac	tca	aca	cca	gga	att	240
Val	Pro	Ala	Thr	Ser	Pro	Thr	Pro	Leu	Ser	Asp	Ser	Thr	Pro	Gly	Ile	
65					70					75					80	
att	gat	gat	att	tta	aca	gta	agg	ttc	acg	aca	gac	tac	ttt	gaa	gta	288
Ile	Asp	Asp	Ile	Leu	Thr	Val	Arg	Phe	Thr	Thr	Asp	Tyr	Phe	Glu	Val	
			85					90					95			
agc	agc	aag	aaa	gat	atg	gtt	gaa	gag	tct	gag	gcg	gga	agg	gga	act	336
Ser	Ser	Lys	Lys	Asp	Met	Val	Glu	Glu	Ser	Glu	Ala	Gly	Arg	Gly	Thr	
			100					105					110			
gag	acc	tct	ctt	cca	aat	gtt	cac	cat	agc	tca	tga					372
Glu	Thr	Ser	Leu	Pro	Asn	Val	His	His	Ser	Ser						
		115					120									

<210> 44
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 44

Met	Lys	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Met	Leu	Val	Leu	Leu	Pro	Gln	
1				5					10					15		
Val	Ile	Pro	Ala	Tyr	Ser	Gly	Glu	Lys	Lys	Cys	Trp	Asn	Arg	Ser	Gly	
			20					25					30			
His	Cys	Arg	Lys	Gln	Cys	Lys	Asp	Gly	Glu	Ala	Val	Lys	Asp	Thr	Cys	
		35					40					45				
Lys	Asn	Leu	Arg	Ala	Cys	Cys	Ile	Pro	Ser	Asn	Glu	Asp	His	Arg	Arg	
	50					55					60					
Val	Pro	Ala	Thr	Ser	Pro	Thr	Pro	Leu	Ser	Asp	Ser	Thr	Pro	Gly	Ile	
65					70					75					80	
Ile	Asp	Asp	Ile	Leu	Thr	Val	Arg	Phe	Thr	Thr	Asp	Tyr	Phe	Glu	Val	
			85					90						95		

Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr
100 105 110

Glu Thr Ser Leu Pro Asn Val His His Ser Ser
115 120

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 45
aggttgagta tttgccagac 20

<210> 46
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 46
aggacagggg tgagtgata 19

<210> 47
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(246)
<223> Coding sequence for the variant human DEFB126 gene

<400> 47
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
20 25 30

att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt 144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
35 40 45

tgg gca atg tgc ggc aaa ggg act gct gtg ttc cag ctg aca gac gtg 192

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
 50 55 60

cta att atc ctg ttt tct gtg tcc aga caa aga cta caa gaa ttt caa 240
 Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
 65 70 75 80

cag taa 246
 Gln

<210> 48
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 48

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1 5 10 15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
 20 25 30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
 35 40 45

Trp Ala Met Cys Gly Lys Gly Thr Ala Val Phe Gln Leu Thr Asp Val
 50 55 60

Leu Ile Ile Leu Phe Ser Val Ser Arg Gln Arg Leu Gln Glu Phe Gln
 65 70 75 80

Gln

<210> 49
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(336)
 <223> Coding sequence of the human DEFB126 gene

<400> 49
 atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
 Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
 1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga	96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly	
20 25 30	
att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt	144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	
tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga	192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	
50 55 60	
cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att	240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	
65 70 75 80	
tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act	288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr	
85 90 95	
gct tcg atg tct tcg atg gct cct acc ccc gtt tct ccc act ggt tga	336
Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly	
100 105 110	

<210> 50
 <211> 111
 <212> PRT
 <213> Homo sapiens
 <400> 50

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln	
1 5 10 15	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly	
20 25 30	
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	
50 55 60	
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	
65 70 75 80	
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr	
85 90 95	

Ala Ser Met Ser Ser Met Ala Pro Thr Pro Val Ser Pro Thr Gly
100 105 110

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 51
aatggtgaga aagatgacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 52
gttgaatgga gggaaagt 18

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequencing primer

<400> 53
gtaggtatatt atgattag 18

<210> 54
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(333)
<223> Coding sequence for the variant human DEFB126 gene

<400> 54
atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa 48
Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
1 5 10 15

ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga 96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly

	20	25	30	
att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt				144
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly				
	35	40	45	
tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga				192
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg				
	50	55	60	
cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att				240
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile				
	65	70	75	80
tca aca gta aca gca aca aca gca aca aca act ttg atg atg act act				288
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr				
	85	90	95	
gct tcg atg tct tcg atg gct cct acc cgt ttc tcc cac tgg ttg a				334
Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu				
	100	105	110	

<210> 55
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 55

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln				
1	5	10	15	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly				
	20	25	30	
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly				
	35	40	45	
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg				
	50	55	60	
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile				
	65	70	75	80
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr				
	85	90	95	
Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu				
	100	105	110	

<210> 56
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic snapshot primer

<400> 56
ttttttttttt tttttttttt tttttttttt tttgctcaat ggctttctct 50